CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2011 SUPPLEMENT

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Section numbers given is this supplement are only approximate.

Add to Designators:

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Morphological and Physiological Traits

Pre-harvest Sprouting

QTL

Argent (non-dormant, white seeded) / W98616 (dormant, white seeded): 90 DH lines: Strong QTLs on chromosomes 1A, 3A, 4A and 7A and weaker QTLs on 2B, 5B, and 6B, all from W98616 {10740}.

XX.Embryo Lethality

XX.1.Embryo lethality in wheat x rye hybrids

The Chinese Spring (Imperial rye) addition lines 6R and 6RL crossed with different inbred rye lines (R2, R6, R7) produced hybrid seeds with different proportions of differentiated embryos. R2 with (*Eml-R1a*) gave only undifferentiated embryos; R6 and R7 (with *Eml-R1b*) gave 74-100% differentiated embryos {10748}. Crosses of R2 with the CS nulli-tetrasomics gave differentiated embryos only with N6AT6B and N6AT6D, indicating the presence of a complementary factor *Eml-A1* chromosome 6A {10748}.

39.Height

39.2. Reduced Height : GA-sensitive

***Rht14*.**	6AS {10767}.	**ma:**	*Rht14* – 11.7 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht16* and *Rht18* {10767}.			
Rht16.	6AS {10767}.	m**a:**	*Rht16* – 28.0 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht14* and *Rht18* {10767}.			
Rht18.	6AS {10767}.	m**a:**	*Rht18* – 25.1 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht14* and *Rht16* {10767}.			

43.Lack of Ligules

***lg1*.**	, 2BS {10767}.

XX.Lesion Mimicry

Lesion mimics that resemble the responses of plants to infection by pathogens have occur in many species ({10743} for examples).

lm {10743}.	1BL {10743}.	**bin:**	C1BL6-0.32 {10743}.
v:	Ning 7840 {10743}.	**ma:**	Proximal to *Xgwm264.1-1B* {10743}.
Lm was positively associated with *QLr.pser.1BL* {10743}.			

XX.Soft Glumes

sog.	**bin:**	C-2AS5-0.78.	**dv:**	Tm-9, a mutant of TA4342-96 {10769}.

	ma:	*Xgwm71-2A* – 3.3 cM – *sog* – 3.5 cM – *Xbcd120-2A* {10769}.
Sog.	**dv:**	*T. monococcum* ssp. *aegilopoides* TA4342-96 {10769}.

Replace the previous entry regarding the relationship to Tenacious Glumes with: 'The Soft Glume locus is not an orthologue of Tenacious Glumes {10769}'.

69.Stem Solidness

***Qsst.msub-3BL*.** Add following the current entry:
Stem solidness in chromosome 3B of Golden Ball was verified in Langdon-Golden Ball disomic substitution lines {10730}.

71.Tenacious Glumes

Tg1.	**bin:**	2BS-3 1.00-0.84.
Tg2.	**v:**	TA 3419 = *Tetra Canthatch / Ae. tauschii* ssp. *meyeri* TA1599 {10769}..
	ma:	*Xgwm261/Xwmc503-2D* – 2.3 cM – *Tg2* – 5.9 cM – *Xfba88/Xfbc400-2D* {10769}.

Replace the note on the relationship with Soft Glumes with: 'The Tenacious Glume loci are not orthologues of the Soft Glume locus {10769}'.

75.Yield and Yield Components

75.1.2. 1000-grain weight

TaCwi-A1{10812}.	**ma:**	*Xbarc15* – 10.9 cM –*TaCwi-A1*-STS markers Cwi21 and Cwi22 – 17.6 cM – *Xgwm71-2AL* {10812}.

Based on the rice *GIF1* gene encoding a cell wall invertase (GenBank accession EU095553), common wheat *TaCwi-A1* was cloned, and two STS markers Cwi21 and Cwi22 were developed from the polymorphisms between two allelic variants. On average, *TaCwi-A1a* had 1,000 grain weights 2.4 g higher than *TaCwi-A1b* {10812}.

TaGW2-6A {10781}.	**ma:**	*Xcfd80-6AS.2* – 0.6 cM – *TaGW2-CAPS* – 0.5 cM – *Xbarc146-6A.1/Xwms132.4-6A* {10781}.

Based on its *OsGW2* orthologue in rice this gene was characterized and mapped as a CAPS marker in wheat {10781}. SNPs in the promoter region allowed distinction of two haplotypes. Hap-6A-A was mainly present in southern Chinese wheats; Hap6A-G was present in varieties from central and eastern Europe. On average Hap-6A-A had 1,000 grain weights more than 3g higher than Hap-6A-G {10781}.

75.12. Spike number per plant

QSn.sdau-BL {10784}.	**ma:**	*Xwmc657-4B* – 4.6 cM – *QSn.sdau-4B* – 1.6 cM – *Xgwm495-4B* {10784}.

QSn.sdau-BL was resolved as a single gene in Line 05210/Laizhou 953 {10784}. It was associated with decreased spike length and grain number per spike.

Proteins

79.5.6. Waxy proteins

***Wx-A1*.**				
	Wx-A1h {10763}.	Null allele.	**tv:**	Buck Topacio {10763}.
This is probably a unique allele possessing a 1 bp deletion in exon 6 leading to frameshift and a stop codon: partial sequence GQ120523 {10763}.				

Wx-B1. At the end of section add:
A dominant PCR marker for identifying heterozygotes at the *Wx-B1* locus is reported in {10732}.

79.5.8. Puroindolines and grain softness protein

Add note:
Lines possessing the alien-derived genes *Lr57* and *Yr40* lack puroindoline genes and therefore should be hard phenotypes {10770}.

79.5.12. Serine proteinase inhibitors

Serine proteinase inhibitors or serpins are salt soluble proteins (~43 kDa) representing about 4% of the total protein in wheat and barley endosperms. They may have a role in plant defense.

Srp-A1 {10754}.		5AL {10754}.	
Srp-B1 {10754}.		*Srp5B* {10754}.	5BL {10754}.
	Srp-B1a {10754}.	*Srp5Ba* {10754}.	
	v:	Etawah {10755}; Federation {10755}; Frame {10755}; Pugsley {10754}; Stylet {10755}.	
	Srp-B1b {10754}.	Null allele.	
	v:	Correll {10755}; EGA Eagle Rock {10755}; Gladius 10755}; Yitpi {10755}.	
	This allele reduced milling yield by 0.4% {10755}.		
Srp-D1 {10754}.	5DL {10754}.		

79.3. Endosperm storage proteins

79.3.1. Glutenins

79.3.1.1. Glu-1

Glu-A1

Restore the following entries erroneously deleted in a previous update:

Glu-A1v {10327}.	2.1*{10327}.	**v:**	KU-1094 {10327}; KU-1026 {10327}; KU-1086 {10327}; Grado {10327}, KU-1139 {10327}.
Glu-A1w [{10327}].	2'{10327}.	**v:**	TRI14165/91 {10327}.

Add:

Glu-A1z {10805}.	[*Glu-A1^{m}a* {10805}].		
	dv: PI 191146, *T. monococcum*. ssp. *monococcum* {10805}.		
Glu-A1aa {10805}.	[*Glu-A1^{m}b* {10805}].		
	dv: PI 190946, *T. monococcum* L. ssp. *monococcum* {10805}.		
Glu-A1ab {10805}.	[*Glu-A1^{m}c* {10805}].		
	dv: PI 191098, *T. monococcum* ssp. *monococcum* {10805}.		
Glu-A1ac {10806}.	[*Glu-A^{u}1-I* {10806}].	**dv:**	PI 428319, {10806}.
Glu-A1ad {10806}.	[*Glu-A^{u}1-II* {10806}].	**dv:**	PI 428232 {10806}.
Glu-A1ae {10806}.	[*Glu-A^{u}1-III* {10806}].	**dv:**	PI 428240 {10806}.
Glu-A1af {10806}.	[*Glu-A^{u}1-IV* {10806}].	**dv:**	PI 428335 {10806}.
Glu-A1ag {10806}.	[*Glu-A^{u}1-V* {10806}].	**dv:**	PI 538741 {10806}.
Glu-A1ah {10806}.	[*Glu-A^{u}1-VI* {10806}].	**dv:**	PI 428230 {10806}.
Glu-A1ai {10806}.	[*Glu-A^{u}1-VII* {10806}].	**dv:**	PI 428253 {10806}.
Glu-A1aj {10806}.	[*Glu-A^{u}1-VIII* {10806}].	**dv:**	PI 427328 {10806}.
Glu-A1ak {10806}.	[*Glu-A^{u}1-IX* {10806}].	**dv:**	PI 428327 {10806}.
Glu-A1al {10806}.	[*Glu-A^{u}1-X* {10806}].	**dv:**	PI 428256 {10806}.
Glu-A1am {10806}.	[*Glu-A^{u}1-XI* {10806}].	**dv:**	PI 428224 {10806}.
Glu-A1an {10806}.	[*Glu-A^{u}1-XII* {10806}].	**dv:**	PI 428228 {10806}.
Glu-A1ao {10806}.	[*Glu-A^{u}1-XIII* {10806}].	**dv:**	PI 538724 {10806}.
Glu-A1ap {10806}.	[*Glu-A^{u}1-XIV* {10806}].	**dv:**	TRI 6734 {10806}.
Glu-A1aq {10806}.	[*Glu-A^{u}1-XV* {10806}].	**dv:**	TRI 11494 {10806}.
Glu-A1ar {10806}.	[*Glu-A^{u}1-XVI* {10806}].	**dv:**	TRI 11495 {10806}.
Glu-A1as {10806}.	[*Glu-A^{u}1-XVII* {10806}].	**dv:**	PI 428217 {10806}.
Glu-A1at {10806}.	[*Glu-A^{u}3-XVIII* {10806}].	**dv:**	PI 428225 {10806}.
Glu-A1au {10806}.	[*Glu-A^{u}3-XIX* {10806}].	**dv:**	PI 538733 {10806}.
Glu-A1av {10806}.	[*Glu-A^{u}3-XX* {10806}].	**dv:**	PI 428196 {10806}.
Glu-A1aw {10806}.	[*Glu-A^{u}3-XXI* {10806}].	**dv:**	PI 538724 {10806}.
Glu-A1ax {10806}.	[*Glu-A^{u}3-XXII* {10806}].	**dv:**	PI 428191 {10806}.
Glu-A1ay {10806}.	[*Glu-A^{u}3-XXIII* {10806}].	**dv:**	TRI 6734 {10806}.
Glu-A1az {10806}.	[*Glu-A^{u}3-XXIV* {10806}].	**dv:**	TRI 11496 {10806}.

Glu-B1

Amendment:

Glu-B1al. Replace '7+8*' with '7^{OE}+7^{OE}+8*'. Add {899} after 'Glenlea'.

Add to the existing note:

However, there is evidence that over-expression is due to duplication of subunit 7 {10196}. In regard to subunit 8*, evidence was presented to indicate that in Glenlea, one of the standard cultivars for the allele, this subunit is the same as subunit 8 {10808}.

Add:

Glu-B1br {10807}.	7.1+7.2+8* {10807}.	**v:**	H45 {10807}.
Glu-B1bs {10807}.	7.3+7^{OE}+ 8* {10807}.	**v:**	VQ0437 {10807}.
Glu-B1bt {10809}.	17'+18' {10809}.	**tv:**	TGR-214 {10809}.
Glu-B1bu {10809}.	17'+18* {10809}.	**tv:**	TGR-2246 {10809}.
Glu-B1bv {10809}.	13**+8* {10809}.	**tv:**	TGR-003 {10809}.
Glu-B1bw {10809}.	8' {10809}.	**tv:**	TGR-244 {10809}.
Glu-B1bx {10810}.	7+17 {10810}.	**v:**	CWI-59797, *T. aestivum* var. *ferrugineum* {10810}.
Glu-B1by {10808}.	7b*+8 {10808}.	**v:**	Eshimashinriki {10808}.
Glu-B1bz {10808}.	7^{OE} {10808}.	**v:**	Darius {10808}; Cappelle-Desprez {10808}; Festin {10808}; Petrel {10808}; Attila {10808}.
Glu-B1ca {10808}.	6+8b* {10808}.	**v:**	Nidera Baguette 10 {10808}; Apollo {10808}; Brimstone {10808}; Clément {10808}; Ruso {10808}; Pepital {10808}; Thesee {10808}.
Glu-B1cb {10808}.	7^{OE}+8 {10808}.	**v:**	Demai 3 {10808}; ACA 303 {10808}; Courtot {10808}; Shinchunaga {10808}.
Glu-B1cc {10808}.	7^{OE}+8a* {10808}.	**v:**	Pioneer {10808}; Klein Jabal 1 {10808}; ProINTA Redemón {10808}.
Glu-B1cd {10808}.	7^{OE}+8b* {10808}.	**v:**	ACA 601 {10808}.
Glu-B1ce {10808}.	7+8a* {10808}.	**v:**	Tasman {10808}; Jing 411 {10808}.

Glu-D1

Add:

Glu-D1bu {10810}.	2'+12 {10810}.	**v:**	CWI-64806, *T. aestivum* var. *aestivum* {10810}.
Glu-D1bv {10810}.	2''+10 {10810}.	**v:**	CWI-65297, *T. aestivum* var. *erythroleucon* {10810}.
Glu-D1bw {10810}.	2''+12 {10810}.	**v:**	CWI-60509, *T. aestivum* var. *graecum* {10810}.

Glu-B1-1

Add:

Glu-B1-1ah {899}.		7^{OE} {899}.			
	v:	Benkuti 1201{10196, 10197}; Glenlea {899}; Klein Universal II{10196}; Tezanos Pintos Precoz {10196}; Tobari 66{10196}.			
Glu-B1-1ai {10807}.		7.1 {10807}.	**v:**	H45 {10807}.	
Glu-B1-1aj {10807}.		7.2 {10807}.	**v:**	H45 {10807}.	
Glu-B1-1ak {10807}.		7.3 {10807}.	**v:**	VQ0437 {10807}.	
Glu-B1-1al {10809}.		17’ {10809}.	**tv:**	TGR-214{10809}; TGR-2246 {10809}.	
Glu-B1-1am {10809}.		13** {10809}.	**tv:**	TGR-003 {10809}.	
Glu-B1-1an {10808}.		7b* {10808}.	**v:**	Eshimashinriki {10808}.	

Glu-B1-2

Add:

Glu-B1-2ai {10809}.		8’ {10809}.	**tv:**	TGR-244 {10809}.
Glu-B1-2aj {10808}.		8a* {10808}.	**v:**	Pioneer {10808}; Jing 411 {10808}; Tasman {10808}.
Glu-B1-2ak {10808}.		8b* {10808}.	**v:**	Nidera Baguette 10 {10808}; ACA 601 {10808}.

Glu-A3

Replace:

Glu-A3g {00113,00114}.		6+10+20 {00114}.	**v:**	Glenlea {10185}.
	tv:	Claro de Balazote.		
with:				
Glu-A3g {00113}	**v:**	Glenlea {10185}.		

Add:

Glu-A3r {03116}.	[*Glu-A3d'* {03116}].		
	v:	Magistral hexaploid triticale {03116}.	
Glu-A3s {00114}.	[*Glu-A3g* {00114}].	6+10+20 {00114}.	
	tv:	Claro de Balazote {00114}.	
Glu-A3t {10805}.	*Glu-A3^{m}a* {10805}.		
	dv:	PI 190947, *T. monococcum* ssp. *monococcum* {10805}.	
Glu-A3u {10805}.	*Glu-A3^{m}b* {10805}.		
	dv:	PI 190946, *T. monococcum* ssp. *monococcum* {10805}.	
Glu-A3v {10805}.	*Glu-A3^{m}c* {10805}.		
	dv:	BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.	
Glu-A3w {10805}.	*Glu-A3^{m}d* {10805}.		
	dv:	PI 191097, *T. monococcum* ssp. *monococcum* {10805}.	
Glu-A3x {10805}.	*Glu-A3^{m}e* {10805}.		
	dv:	BGE-013624, *T. monococcum* ssp. *monococcum* {10805}.	

Glu-A3y {10805}.	*Glu-A3^{m}f* {10805}.		
	dv:	PI 191094, *T. monococcum* ssp. *monococcum* {10805}.	
Glu-A3z {10806}.	*Glu-A^{u}3-I* {10806}.	**dv:**	PI 428319, *T. urartu* {10806}.
Glu-A3aa {10806}.	*Glu-A^{u}3-II* {10806}.	**dv:**	PI 428327, *T. urartu* {10806}.
Glu-A3ab {10806}.	*Glu-A^{u}3-III* {10806}.	**dv:**	PI 428340, *T. urartu* {10806}.
Glu-A3ac {10806}.	*Glu-A^{u}3-IV* {10806}.	**dv:**	PI 428322, *T. urartu* {10806}.
Glu-A3ad {10806}.	*Glu-A^{u}3-V* {10806}.	**dv:**	PI 428188, *T. urartu* {10806}.
Glu-A3ae {10806}.	*Glu-A^{u}3-VI* {10806}.	**dv:**	PI 428203, *T. urartu* {10806}.
Glu-A3af {10806}.	*Glu-A^{u}3-VII* {10806}.	**dv:**	PI 428255, *T. urartu* {10806}.
Glu-A3ag {10806}.	*Glu-A^{u}3-VIII* {10806}.	**dv:**	PI 428328, *T. urartu* {10806}.
Glu-A3ah {10806}.	*Glu-A^{u}3-IX* {10806}.	**dv:**	PI 428256, *T. urartu* {10806}.
Glu-A3ai {10806}.	*Glu-A^{u}3-X* {10806}.	**dv:**	PI 428217, *T. urartu* {10806}.
Glu-A3aj {10806}.	*Glu-A^{u}3-XI* {10806}.	**dv:**	PI 428335, *T. urartu* {10806}.
Glu-A3ak {10806}.	*Glu-A^{u}3-XII* {10806}.	**dv:**	PI 428186, *T. urartu* {10806}.
Glu-A3al {10806}.	*Glu-A^{u}3-XIII* {10806}.	**dv:**	PI 428183, *T. urartu* {10806}.
Glu-A3am {10806}.	*Glu-A^{u}3-XIV* {10806}.	**dv:**	TRI 11563, *T. urartu* {10806}.
Glu-A3an {10806}.	*Glu-A^{u}3-XV* {10806}.	**dv:**	PI 427328, *T. urartu* {10806}.
Glu-A3ao {10806}.	*Glu-A^{u}3-XVI* {10806}.	**dv:**	PI 428253, *T. urartu* {10806}.
Glu-A3ap {10806}.	*Glu-A^{u}3-XVII* {10806}.	**dv:**	PI 538735, *T. urartu* {10806}.
Glu-A3aq {10806}.	*Glu-A^{u}3-XVIII* {10806}.	**dv:**	PI 428225, *T. urartu* {10806}.
Glu-A3ar {10806}.	*Glu-A^{u}3-XIX* {10806}.	**dv:**	PI 538733, *T. urartu* {10806}.
Glu-A3as {10806}.	*Glu-A^{u}3-XX* {10806}.	**dv:**	PI 428196, *T. urartu* {10806}.
Glu-A3at {10806}.	*Glu-A^{u}3-XXI* {10806}.	**dv:**	PI 538724, *T. urartu* {10806}.
Glu-A3au {10806}.	*Glu-A^{u}3-XXII* {10806}.	**dv:**	PI 428191, *T. urartu* {10806}.
Glu-A3av {10806}.	*Glu-A^{u}3-XXIII* {10806}.	**dv:**	TRI 6734, *T. urartu* {10806}.
Glu-A3aw {10806}.	*Glu-A^{u}3-XXIV* {10806}.	**dv:**	TRI 11496, *T. urartu* {10806}.

Glu-B3

Add:

Glu-B3ab {10804}.	**v:**	Hope {10804}; Nanbukomugi {10804}.
Glu-B3ac {10804}.	**v:**	Thesee {10804}; ACA 801 {10804}; Klein Proteo {10804}.
Glu-B3ad {10804}.	**v:**	AC Vista {10804}; Heilo {10804}; Opata85 {10804}; Ruso {10804}.

Glu-D3

In the ***Glu-D3d*** entry, add 'Jufy-1 {10813}' to the standard stock list.

Add:

Glu-D3l {10804}.	**v:**	Heilo {10804}; Jing411 {10804}, Pepital {10804}; Thesee {10804}.
Glu-D3m {10804}.	**v:**	Darius {10804}.

79.3.2. Gliadins

79.3.2.1. Gli-1

Gli-A1

In the appropriate entry, replace:
Gli-A1null with ***Gli-A1w*** and add a column stating 'null allele'.

Add:

Gli-A1x {10805}.	[*Gli-A1^{m}a* {10805}].		
	dv: PI 191146, *T. monococcum* ssp. *monococcum* {10805}.		
Gli-A1y {10805}.	[*Gli-A1^{m}b* {10805}].		
	dv: PI 190947, *T. monococcum* ssp. *monococcum* {10805}.		
Gli-A1z {10805}.	[*Gli-A1^{m}c* {10805}].		
	dv: PI 190946, *T. monococcum* ssp. *monococcum* {10805}.		
Gli-A1aa {10805}.	[*Gli-A1^{m}d* {10805}].		
	dv: PI 191097, *T. monococcum* ssp. *monococcum* {10805}.		
Gli-A1ab {10805}.	[*Gli-A1^{m}e* {10805}].		
	dv: BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.		
Gli-A1ac {10805}.	[*Gli-A1^{m}f* {10805}].		
	dv: BGE-013626, *T. monococcum* ssp. *monococcum* {10805}.		
Gli-A1ad {10805}.	[*Gli-A1^{m}g* {10805}].		
	dv: BGE-013628, *T. monococcum* ssp. *monococcum* {10805}.		
Gli-A1ae {10811}.	[*Gli-A^{u}1-I* {10811}].	**dv:**	PI-428333, *T. urartu* {10811}.
Gli-A1af {10811}.	[*Gli-A^{u}1-II* {10811}].	**dv:**	PI-428319, *T. urartu* {10811}.
Gli-A1ag {10811}.	[*Gli-A^{u}1-III* {10811}].	**dv:**	PI-428335, *T. urartu* {10811}.
Gli-A1ah {10811}.	[*Gli-A^{u}1-IV* {10811}].	**dv:**	PI-428323, *T. urartu* {10811}.
Gli-A1ai {10811}.	[*Gli-A^{u}1-V* {10811}].	**dv:**	PI-428231, *T. urartu* {10811}.
Gli-A1aj {10811}.	[*Gli-A^{u}1-VI* {10811}].	**dv:**	PI-428194, *T. urartu* {10811}.
Gli-A1ak {10811}.	[*Gli-A^{u}1-VII* {10811}].	**dv:**	PI-428256, *T. urartu* {10811}.
Gli-A1al {10811}.	[*Gli-A^{u}1-VIII* {10811}].	**dv:**	PI-428234, *T. urartu* {10811}.
Gli-A1am {10811}.	[*Gli-A^{u}1-IX* {10811}].	**dv:**	PI-428320, *T. urartu* {10811}.
Gli-A1an {10811}.	[*Gli-A^{u}1-X* {10811}].	**dv:**	PI-428255, *T. urartu* {10811}.
Gli-A1ao {10811}.	[*Gli-A^{u}1-XI* {10811}].	**dv:**	PI-428241, *T. urartu* {10811}.
Gli-A1ap {10811}.	[*Gli-A^{u}1-XII* {10811}].	**dv:**	PI-428235, *T. urartu* {10811}.
Gli-A1aq {10811}.	[*Gli-A^{u}1-XIII* {10811}].	**dv:**	PI-428183, *T. urartu* {10811}.
Gli-A1ar {10811}.	[*Gli-A^{u}1-XIV* {10811}].	**dv:**	PI-428317, *T. urartu* {10811}.
Gli-A1as {10811}.	[*Gli-A^{u}1-XV* {10811}].	**dv:**	PI-427328, *T. urartu* {10811}.
Gli-A1at {10811}.	[*Gli-A^{u}1-XVI* {10811}].	**dv:**	PI-428327, *T. urartu* {10811}.
Gli-A1au {10811}.	[*Gli-A^{u}1-XVII* {10811}].	**dv:**	PI-428253, *T. urartu* {10811}.
Gli-A1av {10811}.	[*Gli-A^{u}1-XVIII* {10811}].	**dv:**	PI-428224, *T. urartu* {10811}.
Gli-A1aw {10811}.	[*Gli-A^{u}1-XIX* {10811}].	**dv:**	PI-538727, *T. urartu* {10811}.
Gli-A1ax {10811}.	[*Gli-A^{u}1-XX* {10811}].	**dv:**	PI-428211, *T. urartu* {10811}.
Gli-A1ay {10811}.	[*Gli-A^{u}1-XXI* {10811}].	**dv:**	PI-538724, *T. urartu* {10811}.

Gli-A1az {10811}.	[*Gli-A^{u}1-XXII* {10811}].	**dv:**	PI-428191, *T. urartu* {10811}.
Gli-A1ba {10811}.	[*Gli-A^{u}1-XXIII* {10811}].	**dv:**	TRI-6735, *T. urartu* {10811}.
Gli-A1bb {10811}.	[*Gli-A^{u}1-XXIV* {10811}].	**dv:**	TRI-11494, *T. urartu* {10811}.
Gli-A1bc {10811}.	[*Gli-A^{u}1-XXV* {10811}].	**dv:**	TRI-6734, *T. urartu* {10811}.
Gli-A1bd {10811}.	[*Gli-A^{u}1-XXVI* {10811}].	**dv:**	TRI-11496, *T. urartu* {10811}.

Gli-B1
In the appropriate entry, replace:
Gli-B1null with ***Gli-B1x*** and add a column stating 'null allele'.

Gli-D1
In the appropriate entry, replace:
Gli-D1null with ***Gli-D1o*** and add a column stating 'null allele'.

79.3.2.2. Gli-2

Gli-A2

In the appropriate entry, replace:
Gli-A2null with ***Gli-A2aj*** and add a column stating 'null allele'.

Add:

Gli-A2ak {10805}.	[*Gli-A2^{m}a* {10805}].	**dv:**	BGE-013630, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2al {10805}.	[*Gli-A2^{m}b* {10805}].	**dv:**	PI 094740, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2am {10805}.	[*Gli-A2^{m}c* {10805}].	**dv:**	PI 190942, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2an {10805}.	[*Gli-A2^{m}d* {10805}].	**dv:**	PI 190947, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ao {10805}.	[*Gli-A2^{m}e* {10805}].	**dv:**	PI 190946, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ap {10805}.	[*Gli-A2^{m}f* {10805}].	**dv:**	BGE-013626, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2aq {10805}.	[*Gli-A2^{m}g* {10805}].	**dv:**	PI 191095, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ar {10805}.	[*Gli-A2^{m}h* {10805}].	**dv:**	BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2as {10805}.	[*Gli-A2^{m}i* {10805}].	**dv:**	PI 191096, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2at {10805}.	[*Gli-A2^{m}j* {10805}].	**dv:**	BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2au {10805}.	[*Gli-A2^{m}k* {10805}].	**dv:**	BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.

Gli-A2av {10805}.	[*Gli-A2^{m}l* {10805}].	**dv:**	BGE-029108, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2aw {10805}.	[*Gli-A2^{m}m* {10805}].	**dv:**	BGE-013627, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ax {10805}.	[*Gli-A2^{m}n* {10805}].	**dv:**	BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ay {10811}.	[*Gli-A^{u}2-I* {10811}].	**dv:**	PI-428333, *T. urartu* {10811}.
Gli-A2az {10811}.	[*Gli-A^{u}2-II* {10811}].	**dv:**	PI-428320, *T. urartu* {10811}.
Gli-A2ba {10811}.	[*Gli-A^{u}2-II* {10811}].	**dv:**	PI-428230, *T. urartu* {10811}.
Gli-A2bb {10811}.	[*Gli-A^{u}2-IV* {10811}].	**dv:**	PI-428319, *T. urartu* {10811}.
Gli-A2bc {10811}.	[*Gli-A^{u}2-V* {10811}].	**dv:**	PI-428239, *T. urartu* {10811}.
Gli-A2bd {10811}.	[*Gli-A^{u}2-VI* {10811}].	**dv:**	PI-428336, *T. urartu* {10811}.
Gli-A2be {10811}.	[*Gli-A^{u}2-VII* {10811}].	**dv:**	PI-428235, *T. urartu* {10811}.
Gli-A2bf {10811}.	[*Gli-A^{u}2-VIII* {10811}].	**dv:**	PI-428234, *T. urartu* {10811}.
Gli-A2bg {10811}.	[*Gli-A^{u}2-IX* {10811}].	**dv:**	PI-428183, *T. urartu* {10811}.
Gli-A2bh {10811}.	[*Gli-A^{u}2-X* {10811}].	**dv:**	PI-428256, *T. urartu* {10811}.
Gli-A2bi {10811}.	[*Gli-A^{u}2-XI* {10811}].	**dv:**	PI-428255, *T. urartu* {10811}.
Gli-A2bj {10811}.	[*Gli-A^{u}2-XII* {10811}].	**dv:**	PI-428224, *T. urartu* {10811}.
Gli-A2bk {10811}.	[*Gli-A^{u}2-XIII* {10811}].	**dv:**	PI-428208, *T. urartu* {10811}.
Gli-A2bl {10811}.	[*Gli-A^{u}2-XIV* {10811}].	**dv:**	PI-428202, *T. urartu* {10811}.
Gli-A2bm {10811}.	[*Gli-A^{u}2-XV* {10811}].	**dv:**	PI-428217, *T. urartu* {10811}.
Gli-A2bn {10811}.	[*Gli-A^{u}2-XVI* {10811}].	**dv:**	PI-427328, *T. urartu* {10811}.
Gli-A2bo {10811}.	[*Gli-A^{u}2-XVII* {10811}].	**dv:**	PI-428317, *T. urartu* {10811}.
Gli-A2bp {10811}.	[*Gli-A^{u}2-XVIII* {10811}].	**dv:**	PI-428253, *T. urartu* {10811}.
Gli-A2bq {10811}.	[*Gli-A^{u}2-XIX* {10811}].	**dv:**	PI-538742, *T. urartu* {10811}.
Gli-A2br {10811}.	[*Gli-A^{u}2-XX* {10811}].	**dv:**	PI-428232, *T. urartu* {10811}.
Gli-A2bs {10811}.	[*Gli-A^{u}2-XXI* {10811}].	**dv:**	PI-428188, *T. urartu* {10811}.
Gli-A2bt {10811}.	[*Gli-A^{u}2-XXII* {10811}].	**dv:**	PI-428244, *T. urartu* {10811}.
Gli-A2bu {10811}.	[*Gli-A^{u}2-XXIII* {10811}].	**dv:**	PI-538733, *T. urartu* {10811}.
Gli-A2bv {10811}.	[*Gli-A^{u}2-XXIV* {10811}].	**dv:**	PI-428212, *T. urartu* {10811}.
Gli-A2bw {10811}.	[*Gli-A^{u}2-XXV* {10811}].	**dv:**	TRI-6734, *T. urartu* {10811}.
Gli-A2bx {10811}.	[*Gli-A^{u}2-XXVI* {10811}].	**dv:**	PI-428254, *T. urartu* {10811}.

Gli-B2

In the appropriate entry, replace:
Gli-B2null with ***Gli-B2au*** and add a column stating ‘null allele’.

Gli-D2

In the appropriate entry, replace:
Gli-D2null with ***Gli-D2ae*** and add a column stating ‘null allele’.

NEW SECTION: Abiotic Stress Responses

Dehydrin-response Element Binding Factors

DREB proteins are a large family of transcription factors induced by abiotic stresses. Using genome-specific primers an othologous *Dreb1* gene series was placed on chromosomes 3A, 3B and 3D {10729}. SNPs in *Dreb-B1* permitted mapping in chromosome 3BL in the ITMI (Opata 85 / W7984) mapping population.

Dreb-B1 {10729}.	3BL {10729}.		
ma:	*Xmwg818-3B* – 27.3 cM – *Dreb1* – 11.2 cM – *Xfbb117-3B* {10729}.		
Dreb-B1a [{10729}].	**v:**	Opata 85 {10729}.	
Dreb-B1b [{10729}].	**v:**	W7984 {10729}.	

Pathogenic Disease/Pest Reaction

80.Reaction to *Blumeria graminis* DC.

80.1. Designated genes for resistance

Pm4d {10744}.	2AL {10744}.	**bin:**	2AL1-0.85-1.00.		
	dv:	*T. monococcum* Tm27 {10744}.			
	v:	Tm27d2 = WW St 2022 / Tm27 // Amor = TRI 29584 {10744}.			
	ma:	A 218bp fragment was amplified with STS marker *ResPm4* as were other *Pm4* alleles {10744}.			
Pm17.	**v:**	McCormack {10758}; Tribute {10758}; TAM303 {10758}.			
Pm41.	**bin:**	0.63-1.00.			
Pm44 {10790}.	3AS {10790}.	**v:**	Hombar {10790}.		
ma:	Flanked by SSR markers distally located in chromosome 3AS {10790}.				
Pm45 {10791}.	*Pm57-6D* {10790}.	6DS {10791}.			
	v1:	Line NWG0099 {10791}.	**v2:**	D57 {10791}.	
	ma:	Close linkages are reported in the draft manuscript.			

82.Reaction to *Fusarium graminearum*

82.2. Disease: Crown rot caused by *Fusarium pseudograminearum, F. culmorum* and other *Fusarium* species.

Cansas / Ritmo: After *QFHS.whs-5BL* add insert: '(renamed *Qfhs.lfl-1BL* in {10768})'. Then continue at end of the paragraph '*Qfhs.lfl-1BL* was verified in $F_{4:7}$ lines and in detected Biscay, History and Pirat {10768}.

CS / CS(Sumai 3 7A): *QFhb7AC*, nearest marker *Xwmc17-7A*, explained 22% of phenotypic variance for Type II and 24% of phenotypic variance for Type III resistance {10798}.

Lang /*T. spelta* CSCR6: *Qcrs.cpi-3BL* from CSCR6 was flanked by *wPt8438* and *wPt9495*; R^2 up to 0.49, validated in other crosses {10273}. *Qcrs.cpi-4B* from Lang; R^2 up to 0.23 {10273}.

Soissons (relatively resistant) / Orvantis (susceptible): Add at end of paragraph: Increased susceptibility associated with the *Rht-D1b* allele was further confirmed in crosses of semi-dwarf cultivars Apachi, History and Romanus {10793}.

83.Reaction to *Heterodera* avenae Woll.

QCre.pau-1A {10749}.		1AS {10749}.	**dv:**	*T. monococcum* Tm 14087 *QCre.pau-2A* {10749}.
	ma:	*QCre.pau-1A* was mapped in a 3.6 cM interval in a *T. boeoticum* Tb 5088 / Tm 14087 RIL population and was flanked by *Xcfa2153-1A* and *BE444890* {10749}; $R^2 = 0.26$ {10749}.		
QCre.pau-1A was transferred to tetraploid and hexaploid lines {10749}.				
QCre.pau-2A {10749}.		2AS {10749}.	**dv:**	*T. monococcum* Tm 14087 *QCre.pau-1A* {10749}.
	ma:	*QCre.pau-2A* was mapped in a 4.00 cM interval flanked by *BE498358* and *Xwmc358-2A* {10749}; $R^2 = 0.13$ {10749}.		

90. Reaction to *Meloidogyne* spp.

Root knot eelworm

Revise to:

Rkn1 [{632}].		*Rkn* {632}.	6D {10799}.	
		dv:	*Ae. tauschii* G3489.	
		v:	Prosquare, a synthetic hexaploid of Produra/*Ae. tauschii* G3489 {632}.	
Rkn2 [{1621}].		Derived from *Ae. peregrine* (*variabilis*) {1621}.		*Rkn-mn1* {1621}.
	3B{590}.	**v:**	X8 = CS / *Ae. peregrina* No. 1 // Rescler /3/ Lutin {1620}; X35 {1620,1621}.	
	ma:	Co-segregation with RAPD $OpY16_{1065}$ and close linkage with several markers including *Est-B5* {0103}; converted to SCAR Y16 {10486}; May be the same as *CreY* (see reaction to *Heterodera avenae*) on chromosome $3S^v$ from *Aegilops variabilis* translocated to 3BL {10800}.		

Add:			
Rkn3 {10801}.	Derived from *Ae. ventricosa*.		2NS translocation into 2AS {10801}.
	v:	VPM1, Lassik (PI 653535) {10801}.	
ma:	Resistances to *M. javanica* and *M. incognita* mapped to the 2NS translocation in BC_6F_3 near isogenic lines of Anza (PI 638742), Yecora Rojo, and Express with the 2NS translocation {10801}.		

92.Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

92.1. Genes for resistance

QTL

Add at the end of this section:

A summary of QTL analyses is provided in {10276}.

92.2. Sensitivity to SNB toxin

Insert at the beginning of this section:

A discussion on the origin and role of host-specific toxins is provided in {10276}.

Add:

Tsn1.	**v:**	Forno {10275}.	**tv:**	Add: Some *T. dicoccoides* accessions {10756}.
	dv:	Two *Ae. speltoides* accessions {10756}.		
	c:	*Tsn1* has 8 exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA {10756}.		
tsn1.	**ma:**	Add: This interval was reduced to 0.07 cM between *Xfcp620-5B* and *Xfcp394-5B* {10274}.		
Genotype list in {10274}.				
Snn1.	**bin:**	1BS.sat.18.		
	ma:	*XksuD14.2-1BS* – 0.4 cM – *Snn1/XBE498831/XBF474204* – 0.4 cM – *Xpsp3000-1BS/XBE422980/XBE637568/ZBE605202* {10727}; *XksuD14.2* – 0.34 cM – *Snn1/XBE498831/XBF474204* – 0.12 cM – *XBF29322* – 0.04 cM – *Xpsp3000-1BS/XBE422980/XbE637568/XBF605202* {10727}.		
Snn2.	**ma:**	*XTC253803* – 3.6 cM – *Snn2* – 0.4 cM – *Xcfd-2D* {10274}.		
snn2.	**v:**	Add: Atlas 66 {10274}; Cheyenne {10274}; Chinese Spring {10274}; Jagger {10274]; Opata 85 {10274}; Salamouni {10274}; TAM 105 {10274}.		
Snn3 {10728,10507}**.**		Sensitivity to SnTox3 is dominant {10728}.		
	5BS {10728,10507}.	**bin:**	5BS-6 {10507}.	
	v2:	Grandin *Snn2*{10728,10507}.	**ma:**	*Snn3* – 1.4 cM – *Xcfd20 -5BS* {10507}.

snn3.	**v:**	BR34 {10507}.			
Snn4 {10275}**.**	Sensitivity to SnTox4 is dominant {10275}.			1AS {10275}.	
	bin:	1AS3-0.86-1.00 {10275}.	**v:**	Arina {10275}.	
	ma:	*XBG262267/XBG262975* – 0.9 cM – *Snn4* – 1.6 cM – *Xcfd58.1-1AS* {10275}.			
snn4.	**v:**	Forno {10275}.			

QTL
P91193D1 / P92201D5 RIL population: tested in USA and Australia: *QSng.pur-2DL.1* from P91103D1, R^2 = 0.123 (Indiana) and 0.381 (South Perth); and *QSng.pur-2DL.2* from P92201D5, R^2 = 0.069 (Indiana) and 0.112 (South Perth) {10776}.

94.Reaction to *Puccinia graminis* Pers.

Sr2.	**ma:**	Add: Tightly linked CAPS marker csSr2 based on a SNP proved superior to *Xgwm533-3B* as a marker for *Sr2* {10786}.			
Sr13.	**bin:**	6AL-8**.**	**tv:**	Kronos {10777}; Medora {10777}; Sceptre {10777}.	
	ma:	*CD926040 – Sr13 – BE471213* {10777}.			
A gene in Khapstein/9*LMPG and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance gene mapped in {10778} could not be *Sr13*.					
Sr22.	**bin:**	7AL-0.74-0.86.	**v:**	Recombinant line reported in {10772,10773}.	
	ma:	Multiplex marker cssu22 based on STS markers derived from cloned fragment csIH81 was developed in {10772}. This marker gave positive results for *Sr22* in all recombinant lines including those reported in {10773}.			
Sr38.	Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.				
Sr39.	Add at the beginning of notes:Lines with shortened alien segments are reported in {10741}.				
Sr48.	**ma:**	Replace the first sentence with: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* – 2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}.			
Sr50 [{10745}].	*SrR* {0377}.	1DS {10745}.			
	ad:	CS + Imperial 1R {0377}.	**v:**	Line T6-1 AUS 91434 {10745}.	
	al:	*S. cereale* cv. Imperial.			
	ma:	Line T6-1 retains the rye marker AW2-5 {10745}.			
In rye *Sr50* may be allelic with *Sr31*; however in wheat they can be regarded as separate loci.					

Sr50 is located in a small interstitial segment not detected by GISH. Line T6-1 lacks the *Sec-1* allele from rye {10745}.					
Sr51 {10803}.	Homoeologous group 3 {10803}; $3S^{S}S$ {10803}.				
	3A (3AL.$3S^{S}$S) {10803}.		**v:**	TA5619 {10803}.	
	3B (3BL.$3S^{S}$S) {10803}.		**v:**	TA5620 {10803}.	
	3D (3DL.$3S^{S}$S) {10803}.		**v:**	TA5621 {10803}.	
	3D (3DS-$3S^{S}$S.$3S^{S}$L) {10803}.		**v:**	TA5622 {10803}.	
	al:	*Ae. searsii* TA2355 {10803}.			
	ma:	$3S^{S}$-specific markers are provided in {10803}.			
Sr52 {10774}.	6A (6AS.6V#3L) {10774}.				
	v:	TA5617 {10775}.			
	ma:	6V3- specific EST-STS markers are given in {10775}.			
The seedling response conferred by *Sr52* is temperature-sensitive.					
Sr53{10789}.	Derived from *Ae. geniculata*.			5D {10789}.	
	Ti5DS·5DL-5M^{g}L-5DL {10789}.		**v:**	TA5630 **(**U6154-124) {10789}.	
	T5DL-5M^{g}L·5M^{g}S {10789}.		**v:**	TA5625 **(**U6200-64) {10789}.	
	T5DL-5M^{g}L·5M^{g}S {10789}.		**v:**	TA5643 **(**U6200-117) {10789}.	
		al:	*Ae. geniculata* TA10437 {10789}.		
The three translocation lines are re-engineered derivatives of TA5599 (5DL-5M^{g}L.5M^{g}S {10789}).					
SrCad {10733}.	6DS {10733}.				
	v:	AC Cadillac {10733}; AC Crystal {10733}; AC Foremost {10733}; AC Karma {10733}; AC Taber {10733}; AC 2000{10733}; Peace {10733}; 5700 {10733}.			
	ma:	Lines with *Bt10* {10733}. *Xcfd49-6D* – 7.7 cM – *SrCad* – 1.5 cM – FSD_RSA/*Bt10* – 14.1 cM – *Xbarc301-6D* – 0.8 cM – *Xbarc173-6D* {10733}; *Xcfd49-6D* – 7.2 cM – *SrCad* – 1.8 cM FSD-RSA/*Bt10* – 14 cM – *Xcfd75-6D* {10733}.			
SrR.	Delete current listing.				

95.Reaction to *Puccinia striiformis* Westend.

91.1. Designated genes for resistance to stripe rust

Yr1.	**ma:**	Replace the present entry with: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* –2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* - 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}.
Yr5.	Add note: Allelic with *Yr7* and *YrSp* {10759}.	

Yr7.	Add note: Allelic with *Yr5* and *YrSp* {10759}.				
Yr9.	**v2:**	Brigadier *Yr17* {10785}.			
Yr17.	**v2:**	Brigadier *Yr9* {10785}.			
	ma:	Add: SCAR markers SC-372 and SC-385 were developed in {10796}.			
Yr35.	**ma:**	*Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B* {10780}.			
Yr40.	**ma:**	Add: CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.			
Yr42.	Add note: Associated with *Lr62* {10537}.				
Yr46.	Update to: 4DL.		**bin:**	Distal to 0.56.	
	ma:	Change present entry to: *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}.			
Yr49 {10746}.	Adult plant resistance.		3DS {10746}.		
	bin:	3DS-6 (0.55-1.00).	**v1:**	Avocet S*3 / Chuanmai 18 AUS91433 {10746}.	
	v2:	Chuanmai 18 *Yr18* {10746}.			
	ma:	*Xgpw7321-3D/Yr49* – 1 cM – *Xgwm161-3D* {10746}.			

95.2. Temporarily designated genes for resistance to stripe rust

YrSp.	Add note: Allelic with *Yr5* and *Yr7* {10759}.

95.3. Stripe rust QTLs

Alcedo (R) / Brigadier (S): DH population: Two major QTLs *QPst.jic-2DL* (R^2 up to 0.36) and *QPst.jic-4BL* (R^2 up to 0.29) for percent infection contributed be Alcedo {10785}. A seedling-expressed QTL was located at the same position in 2DL {10774}.

Flinor (R)/ Mingxian 169 (S): Two independent QTLs for high temperature (24/18C) seedling resistance located in chromosome 5BL, designated *QYr-tem-5B.1* (*Xbarc89 – Xgwm67*) and *QYr-tem-5B.2* (*Xbarc140n – Xwmc235*) and R^2 = 0.37 and 0.33, respectively {10797}.

Kukri (MR) / Janz (MR): DH population: Tested with pre- and post-2003 Australian *Pst* races in several environments. *QYr.sun-7B* (Kukri) and *Qyr.sun-7D* (= *Yr18*) (Janz) were consistent over environments; *QYr.sun-1B*, *-5B* and *-6B* were detected in most environments and *QYr.sun-3B* was identified in only one season. Two genes, *QYR.sun-1A* from Janz and *QYr.sun-2A* from Kukri, were detected only with pre- and post-2003 races, respectively, and likely contributed to differential responses of these cultivars to the two groups of races {10751}.

96.Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr10.	**tv:**	Altar 82 {10760}; Russello {10760}.	
	c:	Add: A second CC-NBS-LRR gene, *RGA2*, is required for expression of *Lr10* in tetraploid and hexaploid wheats {10760}.	
Lr12.	**v2:**	Caldwell *Lr14a* {10787}.	
Lr14.			
Lr14a.	**v2:**	Caldwell *Lr12* {10787}.	
Add note at end of section: The *Lr14* region in tetraploid wheat harbours *Qlr.ubo-7B.2*, a gene that confers durable resistance in durums {10734,10736} and that is present in many Italian, CIMMYT and ICARDA durum cultivars {10736}. The relationship of this gene described as *Lr14c* (reference genotype Creso) in {10735} remains to be determined. Reasons for considering Lr14c as a unique allele are given in {10735}. In association mapping the presence of *QLr.ubo-7B.2* was predicted with 96% accuracy based on appropriate alleles of *Xcfa2257.2, Xgwm344.2* and *Xwmc10* in the distal region of chromosome 7BL {10736}.			
Lr17.			
Lr17a.	**ma:**	Add: *Lr17a* – 3.7 cm – *Xbarc212-2a* {10795}.	
Lr18.	Add note: A resistance gene, *LrTt2*, in line 842-2 was located on chromosome 5BL in a similar region to *Lr18*. The claim that *Lr18* and *LrTt2* were different based on different low seedling infection types, but the genetic backgrounds were different {10752}.		
Lr21.	**v:**	Lovitt {10766}; McKenzie {10766}	
	Add to notes: Further haplotype analyses are reported in {10766}.		
Lr25.	**i:**	Tc+Lr25 *Lr48* {10738}.	
	Add note: *Lr25* is closely linked with *Lr48* {10738}.		
Lr35.	Add note at the end of section: Lines with shortened alien segments are reported in {10741}.		

Lr37.	Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.						
Lr39.	2DS {add: ,10731}.						
	ma:	Four markers, *Xbarc124-2D, Xgwm210-2D, Xgdm35-2D* and *Xcfd36-2D* were closely linked with the terminally located *Lr39* (formerly *Lr41*), but the gene order was inconsistent and no specific allele was associated with it {10731}.					
Lr47.	7AS.	**v:**	Add: Bionta 2004 {10737}.				
Lr48.	, 4BS {10738}.	**ma:**	RAPD markers flanking *Lr48* at 2.7 and 8.6 cM are reported in {10738}.				
Lr48 is closely linked with *Lr25* {10738}.							
Lr53.	**ma:**	*Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B* {10780}.					
Lr53 was genetically independent of *Lr36* {10780}.							
Lr57.	**ma:**	Add: CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.					
Lr59.	Add note: Problems in recovering balanced recombinants are reported in {10762}.						
Lr62	Add note: Associated with *Yr42* {10537}.						
Lr67.	**bin:**	Distal to 0.56.					
	ma:	add: *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}.					
LrAlt {10739}.	2AS {10739}.	**v:**	*T. spelta* cv. Altgold {10739}.				
ma:	*LrAlt* – 1.8 cM – *Xbarc212-2A/Xwmc382-2A* – 2 cM – *Xgwm636-2A* {10739}.						
LrWo {10747}.	5B (10747}.	**tv:**	Wollaroi AUS99174 {10747}.				
ma:	*Xgwm234-5B* – 7.2 cM – *LrWo* – 20.3 cM – *wPT-1420* {10747}.						
The relationship of *LrWo* to *Lr52* was not established.							

Complex genotypes: Add:
Coker 9663 *Lr9 Lr10 Lr14a* {10742}
Pioneer 26R61 *Lr13 Lr14b Lr26* {10742}

Genotype lists: French cultivars {10792}. Add to European cultivars {…….,10794}.

96.3. QTLs for reaction to *P. triticina*

Insert above *QLr.sfr-1B*:

QLr.pser.1BL {10743}.	1BL {10743}.	**bin:**	1BL6-0.32 {10743}.
		ma:	Proximal to *Xgwm264.1-1BL* {10743}.

Associated with *lm* producing a lesion mimic phenotype in the absence of disease {10743}.

After the entry for Avocet / Pavon add:
TA 4152-60 (MR) / ND495 (MR): DH population: Five QTL for APR were identified in the field, viz. *QLr.fcu-3AL* (R^2 = 0.18), *QLr.fcu-3BL* (R^2 = 0.19), *QLr.fcu-5BL* (R^2 = 0.07), and *QLr.fcu-6BL* (R^2 = 0.12) from TA 4152-60 and *QLr.fcu-4DL* (R^2 = 0.13) from ND495 {10757}. The 3AL gene also conferred seedling resistance to some races and the 3BL gene conferred resistance to race MFPS {10757}.

Add:
Tetraploid wheat
Association mapping indicated genomic regions affecting leaf rust response in chromosomes 1A, 1B, 2A, 2B (*Lr13, Lr23* region), 3B, 5A, 5B, 6B, 7A and 7B (see *Lr14*) {10736}.

97.Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici-repentis*)

97.1. Insensitivity to tan spot toxin

Tsn.	**dv:**	Two *Ae. speltoides* accessions {10756}.
	tv:	Add: Some *T. dicoccoides* accessions{10756}.
	c:	*Tsn1* has 8 exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA {10756}.

97.3. Resistance to tanspot

TsrAri {10765}.		Recessive.	3A {10765}.
	v:	Arina {10765}; Heines VII {10765}; Zenith {10765}.	

Add: Batavia (S) / Ernie (R): DH population tested over three years. Four (1A (Ernie), 7A, 2BS, 3BS (Batavia)), five (2BS, 5BL (E), 3D, 6A, 7D (B)) and four (2BS, 5BL (E) 1A, 6A (B)) QTL accounted for most of the variation in each year. The greatest effect across years was the QTL on chromosome 2BS (R^2 = 0.382, 0.298 and 0.362, respectively. This QTL was validated in four additional populations {10782}.

Wangshuibai / Ning 7840: RIL population: Race 1: *QTs.ksu-1AS*, R^2 = 0.39 (nearest marker *Xcfa2153-1A*) and *QTs.ksu-2BS*, R^2 = 0.04) (nearest marker *Xbarc2-2B*) {10753}.

XX.Reaction to *Rhizoctonia* spp.

Cause of Rhizoctonia root rot.

Rot1 {10761}.	**v:**	Scarlet-Rz1 {10761}.
Scarlet-Rz1 was produced by mutagenesis {10761}.		

95.Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)

Gb2.	**ma:**	Within the 1R segment: *Gb6* – 15.8 cM – *Gb2*– 11.4 cM – *XIA294* {10764}.		
Gb3.	**v:**	TAM112 (10764}.	**al:**	Insave rye.
Gb6.	**v:**	N96L9970 {10764}.		
	ma:	Within the 1R segment: *Gb6* – 15.8 cM – *Gb2*– 11.4 cM – *XIA294* {10764}.		

101.Reaction to *Tapesia yallundae* (Anomorph: *Pseudocerosporella herpotrichoides*

Add at end of section:

QPch.jic-5A {10771}.	**bin:**	5AL-6; 0.68-0.78.
	ma:	Closely associated with *Xgwm639-5AL* {10771}.

102.Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Bt10.	**v:**	Present in lines with *SrCad* {10733}.

QTL
Blizard (R) / 8405-JC3C (S): DH population. Resistance and markers *Xgwm374-1BS, Xgwm364-1BS* and *Xbarc128-1BS* were within a 3.9 cM interval {10783}.

106.Reaction to Wheat Streak Mosaic Virus

Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosichella*. See: Resistance to colonization by *Eriophyes tulipae*. According to {10226} WSMV may also be seed-borne. At least some sources of resistance to WSMV are also effective against Triticum mosaic virus.

Update:				
Wsm1{379,440}.	Derived from *Th. intermedium*.			
	4D = T4DL.4J^{S}S{391,389}.			
	i:	Karl*4/CI 17884 = PI 583794 = KS93WGRC27{440}.		
	v:	CI 17766 = B-6-37-1{391,800,1543}; CI 17884{391}KS90H445{391}; KS90H450{391}; CI 17883{389}.		
	ad:	CI 17881; CI 17886{391}.		
	su:	4J^{S}S (4A): CI 15092{391}; 4J^{S}S(4D): CI 17882 & CI 17885{391}.		
	ma:	*Wsm1* co-segregated with a STS amplified by the primer set STSJ15{1456}.		
	4D = T4DL.4DS-4J^{S}S {10788}.		**v:**	KS08WGGRC50 {10788}.
	4A {800} = T4AL. 4J^{S}S {391}.			
	6A = T6AS.4J^{S}L + T6AL.4J^{S}S {389}.			

Wsm1 is located in 4J^{S}S (formerly 4Ai#2S). CI 17882, CI 17884, CI 17885 and KS90H445 also carry a 7S *Ae. speltoides* chromosome substituting for 7A (See Reaction to *Schizaphis graminum*)
Wsm1 also confers resistance to Triticum Mosaic Virus {10788}

Wsm2.	3BS (10802}.	**v:**	CO960293-2 {10802}; Snowmass {10802}.
	ma:	*Wsm2* – 5.2 cM – *XSTS3B-55* {10802}; *Xbarc102-3B* – 1.6 cM – *Wsm2* {10802}.	
Wsm2 confers resistance at temperatures below 19C {10802}.			
Wsm3 {10775}.	7B (7BS.7S#3L) {10775}.	**v:**	TA5624 {10775}.

XX.Reaction to Wheat Yellow Mosaic Virus

Vectored by *Polymyxa graminis*. MYMV is closely related to WSSMV, another bymovirus.

YmIb {10750}.	2DL {10750}.	
	v:	Ibis {10750}; Jagger {10750}; KS 831957 {10750}; Madsen {10750}; Yumechikara {10750}.
	ma:	*Xwmc181-2D* – 12.4 cM – *YmIb* – 2.0 cM –*Xcfd16-2D* – 2.0 cM – Xw*mc41-2D* – 3.1 cM – *Xcfd168-2D* {10750}.
The relationships of *YmIb* to previously mapped gene in 2DL for resistance to WYMC and WSSMV in Yangfu 9311 {10258} and a Geneva derivative {0131} were not established		

References

Updates	
10375.	Correct author name from 'Laur' to 'Kaur' and delete 'Draft manuscript'.
10507.	Correct page numbers to 682-693.
10537.	Marais F, Marais A, McCallum B & Pretorius Z 2009 Transfer of leaf rust and stripe rust resistance genes *Lr62* and and *Yr42* from *Aegilops neglecta* Req. ex Bertol. to common wheat. Crop Science 49: 871-879.
10551.	Replace with: Li G, Fang T, Zhang H, Xie C, Li H, Yang T, Nevo E, Fahima T, Sun Q & Liu Z 2009 Molecular identification of a new powdery mildew resistance gene *Pm41* on chromosome 3BL derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). Theoretical and Applied Genetics 119: 531-539.
10564.	58: 1039-1043.
10677.	Update: 2011..*Yr45*, a new wheat gene for stripe rust resistance on the long arm of chromosome 3D. Theoretical and Applied Genetics 122: 189-197.
10678.	Update: Herrera-Foessel SA, Lagudah ES, Huerta-Epino J, Hayden M, Bariana H, Singh D & Singh RP 2011 New slow-rusting leaf rust and stripe rust resistance genes *Lr67* and *Yr46* are pleiotropic or closely linked. Theoretical and Applied Genetics 122: 239-249.

New	
10273.	Ma J, Li HB, Zhang CY, Yang XM, Liu YX, Yan GJ & Liu CJ 2010 Identification and validation of a major QTL conferring crown rot resistance in hexaploid wheat. Theoretical and Applied Genetics 120: 1119-1128.
10274.	Zhang Z, Friesen TL, Simons KJ, Xu SS & Faris JD 2009 Development, identification, and validation of markers for marker-assisted selection against the *Stagonospora nodorum* toxin sensitivity genes *Tsn1* and *Snn2* in wheat. Molecular Breeding 23: 35-49.
10275.	Abeysekara NS, Friesen TL, Keller B & Faris JD 2009 Identification and characterization of a novel-toxin interaction in the wheat-*Stagonospora nodorum* pathosystem. Theoretical and Applied Genetics 120: 117-126.
10276.	Friesen TL, Faris JD, Solomon PS & Oliver RP 2008 Host-specific toxins: effectors of necrotrophic pathogenicity. Cellular Microbiology 10: 1421-1428.
10727.	Reddy L, Friesen TL, Meinhardt SW, Chao SM & Faris JD 2008 Genomic analysis of the *Snn1* locus on wheat chromosome arm 1BS and the identification of candidate genes. The Plant Genome 1: 55-66.
10728.	Friesen TL, Zhang Z, Solomon PS, Oliver RP & Faris JD 2008 Characterization of the interaction of a novel *Stagonospora nodorum* host-selective toxin with wheat susceptibility gene. Plant Physiology 146: 682-693.
10729.	Wei B, Jing RL, Wang CS, Chen JB, Mao XG Chang XP & Jia JZ 2009 *Dreb1* genes in wheat (*Triticum aestivum* L.): development of functional markers and gene mapping based on SNPs. Molecular Breeding 23: 13-22.
10730.	Xu SS, Chu CG, Chao S, Klindworth DL, Faris JD & Elias EM 2010 Marker-assisted characterization of durum wheat Langdon-Golden Ball disomic substitution lines. Theoretical & Applied Genetics 120: 1575-1585.
10731.	Sun XC, Bai GH & Carver BF 2009 Molecular markers for leaf rust resistance gene *Lr41*. Molecular Breeding 23: 311-321.
10732.	Saito M, Vrinten P, Ishikawa G, Graybosch R & Nakamura T 2009 A novel codominant marker for selection of the null *Wx-B1* allele in wheat breeding programs. Molecular Breeding 23:209-217.
10733.	Hiebert CW, Fetch TG, Zegeye T, Thomas JB, Somers DJ, Humphreys DG, McCallum BD, Cloutier S, Singh D & Knott DR 2111 Genetics and mapping of seedling resistance to Ug99 stem rust in Canadian wheat cultivars 'Peace' and 'Cadillac'. Theoretical and Applied Genetics 122: 143-149.
10734.	Maccaferri M, Mantovani P, Tuberosa R, DeAmbrogio E, Giuliani S, Demontis A, Massi A & Sanguineti MC 2008 A major QTL for durable leaf rust resistance widely exploited in durum wheat breeding programs maps on the distal region of chromosome arm 7BL. Theoretical and Applied Genetics 117: 1225-1240.
10735.	Marone D, Del Olmo AI, Laido G, Sillera JC, Emeran AA, Russo MA, Ferragonio P, Giovanniello V, Mazzucotelli E, De Leonardis AM, De Vita P, Blanco A, Cattivelli L, Rubiales D & Mastrangelo AM 2009 Genetic analysis of durable resistance against leaf rust in durum wheat. Molecular Breeding 24: 25-39.
10736.	Maccaferri M, Sanguineti MC, Mantovani P, Demontis A, Massi A, Ammar K, Kolmer JA, Czembor JH, Ezrati S & Tuberosa R 2009 Association mapping of leaf rust response in durum wheat. Molecular Breeding DOI 10.1007/s11032-009-9353-0.

10737.	Bainotti C, Fraschina J, Salines JH, Nisi JE, Dubcovsky J, Lewis SM, Bullrich L, Vanzetti L, Cuniberti M, Campos P, Formica MB, Masiero B, Alberione E & Helguera M 2009 Registration of 'BIOINTA 2004' wheat. Journal of Plant Registrations 3(2): 165-169.
10738.	Samsampour D, Zanjani BM, Pallavi JK, Singh A, Charpe A, Gupta SK & Prabhu KV 2010 Identification of molecular markers linked to adult plant leaf rust resistance gene *Lr48* in wheat and detection of *Lr48* in the Thatcher near-isogenic line with gene *Lr25*. Euphytica 174: 337-342.
10739.	Wang Y, Peng H, Liu G, Xie C, Ni Z, Yang T, Liu Z & Sun Q 2010 Identification and molecular mapping of a leaf rust resistance gene in spelt wheat landrace Altgold. Euphytica 174: 371-375.
10740.	Singh R, Matus-Cadiz M, Baga M, Hucl P & Chibbar RN 2010 Identification of genomic regions associated with seed dormancy in white-grained wheat. Euphytica 174: 391-408.
10741.	Mago R, Zhang P, Bariana H, & Verlin DC. Bansal UK, Ellis JG & Dundas IS 2009 Development of wheat lines carrying stem rust resistance gene *Sr39* with reduced *Aegilops speltoides* chromatin and simple PCR markers for marker-assisted selection. Theoretical and Applied Genetics DOI 10.1007
10742.	Kolmer JA 2010 Genetics of leaf rust resistance in the soft red winter wheat cultivars Coker 9663 and Pioneer 26R61. Plant Disease 94: 628-632.
10743.	Li T & Bai GH 2009 Lesian mimic associates with adult plant resistance to leaf rust infection in wheat. Theoretical and Applied Genetics 119: 13-21.
10744.	Schmolke M, Mohler V, Hartl L, Zeller FJ & Hsam SLK 2010 A novel powdery mildew resistance allele at the *Pm4* locus from einkorn wheat (*Triticum monococcum*). Manuscript.
10745.	Anugrahwati DR, Shepherd KW, Verlin DC, Zhang P, Mirzaghaderi G, Alker E, Francki MG & Dundas IS 2008 Isolation of wheat-rye 1RS recombinants that break the linkage between the stem rust resistance gene SrR and secalin. Genome 51: 341-349.
10746.	Spielmeyer W, et al. 2010. Personal communication.
10747.	Singh B, Bansal UK, Forrest KL, Hayden MJ, Hare RA & Bariana HS 2010 Inheritance and chromosome location of leaf rust resistance in durum wheat cultivar Wollaroi. Euphytica 175: 351-355.
10748.	Tikhenko N, Tsvetkova N, Voylokov A, Dobrovolskaya O, Zaynali K, Nezhad KZ, Röder MS & Börner A 2010 Embryo lethality in wheat x rye hybrids – mode of inheritance and the identification of a complementary gene in wheat. Euphytica 176: 191-198.
10749.	Singh K, Chhuneja P, Singh I, Sharma SK, Garg T, Garg M, Keller B & Dhaliwal HS 2010 Molecular mapping of cereal cyst nematode resistance in *Triticum monococcum* L. and its transfer to the genetic background of cultivated wheat. Euphytica 176: 213-222.
10750.	Nishio Z, Kojima H, Hayata A, Iriki N, Tabiki T, Ito M, Yamauchi H & Murray TD 2010 Mapping a gene conferring resistance to *Wheat yellow mosaic virus* in European winter wheat cultivar 'Ibis' (*Triticum aestivum* L.). Euphytica 176: 223-229.

10751.	Bariana HS, Bansal UK, Schmidt A, Lehmensiek A, Kaur J, Miah H, Howes N & McIntyre CL 2010 Molecular mapping of adult plant stripe rust resistance in wheat and identification of pyramided QTL genotypes. Euphytica 176: 251-260.
10752.	Leonova IN, Budashkina EB, Flath K, Weidner A, Börner A & Röder MS 2010 Microsatellite mapping of a leaf rust resistance gene transferred to common wheat from *Triticum timopheevii*. Cereal Research Communication 38: 211-219.
10753.	Sun XC, Bockus W & Bai GH 2010 Quantitative trait loci for resistance to *Pyrenophora tritici-repentis* race 1 in a Chinese wheat. Phytopathology 100: 468-473.
10754.	Sharp PJ 2010 Personal communication.
10755.	Cane K, Sharp PJ, Eagles HA, Eastwood RF, Hollamby GJ, Kuchel H, Lu M & Martin PJ 2008 The effects on grain quality traits of a grain serpin protein and the VPM1 segment in southern Australian wheat breeding. Australian Journal of Agricultural Research 59: 883-890.
10756.	Faris JD, Zhang Z, Lu H, Lu S, Reddy L, Cloutier S, Fellers JP, Meinhardt SW, Rasmussen JB, Xu SS, Oliver RP, Simons KJ & Friesen TL 2010 A unique wheat disease resistance-like gene governs effector-triggered susceptibility to necrotrophic pathogens. Proceedings of the National Academy of Sciences of USA 107: 13544-13549.
10757.	Chu CG, Friesen TL, Xu SS, Faris JD & Kolmer JA 2009 Identification of novel QTLs for seedling and adult plant leaf rust resistance in a wheat doulbled haploid population. Theoretical and Applied Genetics 119: 263-269.
10758.	Cowger C, Parks R & Marshall D 2009 Appearance of powdery mildew of wheat caused by *Blumeria graminis* f. sp. *tritici* on *Pm17*-bearing cultivars in North Carolina. Plant Disease 93: 1219.
10759.	Zhang P, McIntosh RA, Hoxha S, Dong CM 2009 Wheat stripe rust resistance genes *Yr5* and Yr7 are allelic. Theoretical and Applied Genetics 120: 25-29.
10760.	Loutre C, Wicker T, Travella S, Galli P, Scofield S, Fahima T, Feuillet C, Keller B 2009 Two different CC-NBS-LRR genes are required for *Lr10*-mediated leaf rust resistance in tetraploid and hexaploid wheat. The Plant Journal 60: 1043-1054.
10761.	Okubara PA, Steber CM, DeMacon VL, Walter NL, Paulitz TC, & Kidwell KK 2009 Scarlet-Rz1, an EMS-generated hexaploid wheat with tolerance to the soilborne necrotrophic pathogens *Rhizoctonia solani* AG-8 and *R. oryzae*. Theoretical and Applied Genetics 119: 293-303.
10762.	Marais GF, Kotze L & Ekstein A 2010 Allosyndetic recombinants of the *Aegilops peregrina*- derived *Lr59* translocation in common wheat. Plant Breeding 129: 356-361.
10763.	Vanzetti LS, Pfluger L, Bainotti CT, Jensen C & Helguera M 2010 Identification of a null allele at the *Wx-A1* locus in durum wheat (*Triticum turgidum* L. ssp. *durum* Desf.). Plant Breeding 129: 718-720.
10764.	Lu H, Rudd JC, Burd JD & Weng Y 2011 Molecular mapping of greenbug resistance genes *Gb2* and *Gb6* in 1AL.1RS wheat-rye translocations. Plant Breeding 129: 472-476.
10765.	Tadesse W, Reents HJ, Hsam SLK & Zeller FJ 2010 Monosomic analysis of tanspot resistance gene in the winter cultivar 'Arina'. Plant Breeding 129: 477-479.

10766.	Fu YB, Peterson GW, McCallum BD & Huang L 2010 Population-based resequencing analysis of improved wheat germplasm in wheat leaf rust resistance locus *Lr21*. Theoretical & Applied Genetics 121:271-281.
10767.	Watanabe N. 2008 Genetic collection and development of near-isogenic lines in durum wheat. Vestnik VOGiS 12: 636-643.
10768.	Haberle J, Holzapfel J, Schweizer G & Hartl L 2009 A major QTL for resistance against Fusarium head blight in European winter wheat. Theoretical and Applied Genetics 119: 325-332.
10769.	Sood S, Kuraparthy V, Bai GH & Bill BS 2009 The major threshability genes soft glume (*sog*) and tenacious glume (*Tg*), of diploid and polyploid wheat, trace their origin to independent mutations at non-orthologous loci. Theoretical and Applied Genetics 119: 341-351.
10770.	Kuraparthy V, Sood S, See DR & Gill BS 2009 Development of a PCR assay and marker-assisted transfer of leaf rust and stripe rust rersistance genes *Lr57* and *Yr40* into hard red winter wheats. Crop Science 49: 120-126.
10771.	Burt C, Hollins TW & Nicholson 2011 Identification of a QTL conferring seedling and adult plant resistance to eyespot on chromosome 5A of Cappelle Desprez. Theoretical and Applied Genetics 122: 119-128.
10772.	Periyannan SK, Bansal UK, Bariana HS, Pumphrey M & Lagudah ES 2011 A robust molecular marker for the detection of shortened introgressed segment carrying the stem rust resistance gene *Sr22* in common wheat. Theoretical and Applied Genetics 122: 1-7.
10773.	Olsen E, Brown-Guedira G, Marshall D, Stack E, Bowden RL, Jin Y, Rouse M & Pumphrey MO 2010 Development of lines with a small introgressed segment carrying stem rust resistance gene *Sr22*. Crop Science
10774.	Qi LL, Pumphrey Mo, Friebe B, Qian C, Bowden RL, Rouse MN, Jin Y & Gill BS 2011 A novel Robertsonian event leads to transfer of a stem rust resistance gene (*Sr6V*) effective against race Ug99 from *Dasypyrum villosum* into wheat. Submitted
10775.	Liu W, Seifers DL, Qi LL, Pumphrey MO, Friebe B & Gill BS 2011 A compensating wheat-*Thinoprum intermedium* Robertsonian translocation conferring resistance to wheat streak mosaic virus and Triticum mosaic virus. Manuscript summary provided.
10776.	Uphaus J, Walker M, Shankar H, Golzar H, Loughman R, Francki M & Ohm H 2009 Quantitative trait loci identified for resistance to Stagonospora glume blotch in wheat in the USA and Australia. Crop Science 47: 1813-1822.
10777.	Simons K, Abate Z, Chao SM, Zhang WJ, Rouse M, Jin Y, Elias E & Dubcovsky J 2011 Genetic mapping of stem rust resistance gene *Sr13* in tetraploid wheat (*Triticum turgidum* ssp. *durum* L.) Theoretical and Applied Genetics 122: 649-658.
10778.	Admassu B, Perovic D, Friedt W & Ordan F 2011 Genetic mapping of the stem rust (*Puccinia graminis* f. sp. *tritici* Eriks. & E. Henn) resistance gene *Sr13* in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 122: 6430-648.
10779.	Dubcovsky J, Ordan F, Perovic D, Admassu B, Friedt W, Abate Z, Zhang W & Chao S 2011 Conflicting mapping results for stem rust resistance gene *Sr13*. Theoretical and Applied Genetics 122: 659.

10780.	Dadkhodaie NA, Karaoglou H, Wellings CR & Park RF 2011 Mapping genes *Lr53*and *Yr35* on the short arm of chromosome 6B of common wheat with microsatellite markers and studies of their association with *Lr36*. Theoretical and Applied Genetics 122: 479-487.
10781.	Su ZQ, Hao CY, Wang LF, Dong YC & Zhang ZY 2011 Identification and development of a functional marker of *TaGW2* associated with grain weight in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 122: 211-223.
10782.	Li HB, Yan W, Liu GR, Wen SM & Liu CJ 2011 Identification and validation of quantitative trait loci conferring tan spot resistance in the bread wheat variety Ernie. Theoretical and Applied Genetics 122: 395-403.
10783.	Wang SW, Knox RE, DePauw RM, Clarke FR, Clarke JM & Thomas JB 2009 Markers to a common bunt resistance gene derived from 'Blizzard' wheat (*Triticum aestivum* L.) and mapped to chromosome arm 1BS. Theoretical and Applied Genetics 119: 541-553.
10784.	Deng SM, Wu XR, Wu YY, Zhou RH, Wang HG, Jia JZ & Liu SB 2011 Characterization and precise mapping of a QTL increasing spike number with pleiotropic effects in wheat. Theoretical and Applied Genetics 122: 281-289.
10785.	Jagger LJ, Newell C, Berry ST, MacCormack R & Boyd LA 2011 The genetic characterization of stripe rust resistance in the German wheat cultivar Alcedo. Theoretical and Applied Genetics 122: 723-733.
10786.	Mago R, Simkova H, Brown-Guedira G, Dreisigacker S, Breen J, Jin Y, Singh R, Appels R, Lagudah ES, Ellis J, Dolezel & Spielmeyer W 2011 An accurate DNA marker assay for stem rust resistance gene *Sr2* in wheat. Theoretical and Applied Genetics 122: 635-744.
10787.	Kolmer JA 2009 Genetics of leaf rust resistance in the soft red winter wheat 'Caldwell'. Crop Science 49: 1187-1192.
10788.	Friebe B, Qi LL, Wilson DL, Chang ZJ, Seifers DL, Martin TJ, Fritz AK & Gill BS 2009 Wheat–*Thinopyrum intermedium* recombinants resistant to *wheat streak mosaic virus* and *Triticum mosaic virus*. Crop Science 49: 1221-1226.
10789.	Liu WX, Jin Y, Rouse M, Friebe B, Gill B & Pumphrey MO 2010 Untitled abstract.
10790.	Chen Y, Zhang ZY, Li HJ, Liu ZY, Veisz O, Vida G 2011 *Pm44*, a new gene for powdery mildew resistance on the short arm of wheat chromosome 3A. Draft manuscript.
10791.	Ma HQ et al. 2011. Identification and mapping of a new powdery mildew resistance gene on chromosome 6D of common wheat. Manuscript.
10792.	Goyeau H & Lannou C 2011 Specific resistance to leaf rust expressed at the seedling stage in cultivars grown in France from 1983 to 2007. Euphytica 178: 45-62.
10793.	Holzapfel J, Voss H-H, Miedaner T, Korzun V, Haberle J, Schweizer G, Mohler V & Zimmerman G 2008 Inheritance of resistance to Fusarium head blight in three European winter wheat populations. Theoretical and Applied Genetics 117: 1119-1128.
10794.	Hysing S-C, Singh RP, Huerta-Espino J, Merker A, Liljeroth E & Diaz O 2006 Leaf rust (*Puccinia triticina*) resistance in wheat (*Triticum aestivum*) cultivars grown in Northern Europe 1992-2002. Hereditas 143:1-14.

10795.	Rafiei Boroujeni F, Arzani A, Afshari F &Tobari 2011 Identification and inheritance of leaf rust resistance genes in the wheat cultivar 'Marvdasht'. Cereal Research Communications 39: 67-76.
10796.	Jia JQ, Li GR, Liu C, Lei MP & Yang ZJ 2011 Characterization of wheat yellow rust resistance gene *Yr17* using EST-SSR and rice syntenic region. Cereal Research Communications 39: 88-99.
10797.	Feng J, Zuo LL, Zhang ZY, Lin RM, Cao YY & Xu SC 2011 Quantitative trait loci for temperature-sensitive resistance to *Puccinia striiformis* f. sp. *tritici* in wheat cultivar Flinor. Euphytica 178: 321-329.
10798.	Jayatilake DV, Bai GH & Dong YH 2011 A novel quantitative trait locus for Fusarium head blight resistance in chromosome 7A of wheat. Theoretical and Applied Genetics 122: 1189-1198.
10799.	Kaloshian I, Waines JG, Roberts P, & Thomason IJ 1991 Chromosomal location of root-knot-resistance gene in the D genome of wheat. Journal of Heredity 82: 254-256.
10800.	Coriton O, Barloy D, Huteau V, Lemoine J, Tanguy AM & Jahier J 2009 Assignment of *Aegilops variabilis* Eig chromosomes and translocations carrying resistance to nematodes in wheat. Genome 52:338-346.
10801.	Williamson V & Dubcovsky J 2010 The new resistance gene to root-knot nematodes *Rkn3* is present in the 2NS introgression from *Ae. ventricosa* into common wheat. In preparation.
10802.	Lu HJ, Kottke R, Devkota R, St Amand P, Bernado A, Bai GH, Martin J, Haley S & Rudd J 2011 Molecular mapping of *Wsm2* for wheat streak virus resistance in winter wheat line CO960293-2. Plant & Animal Genome Conf , San Diego, CA.
10803.	Liu WX, Jin Y, Rouse M, Friebe B, Gill B, Pumphrey MO 2011 Development and characterization of wheat-*Ae. searsii* Robertsonian translocations and a recombinant chromosome conferring resistance to stem rust. Theoretical and Applied Genetics, Accepted.
10804.	Liu L, Ikeda TM, Branlard G, Peña RJ, Rogers WJ, Lerner SE, Kolman MA, Xia X, Wang L, Ma W, Appels R, Yoshida H, Wang A, Yan Y & He Z 2010 Comparison of low molecular weight glutenin subunits identified by SDS-PAGE, 2-DE, MALDI-TOF-MS and PCR in common wheat. BMC Plant Biology 2010, 10:124.
10805.	Alvarez JB, Moral A & Martín LM 2006 Polymorphism and genetic diversity for the seed storage proteins in Spanish cultivated einkorn wheat (*Triticum monococcum* L. ssp. *monococcum*). Genetic Resources and Crop Evolution 53: 1061-1067.
10806.	Caballero L, Martín MA & Alvarez JB 2008 Allelic variation for the high- and low-molecular-weight glutenin subunits in wild diploid wheat (*Triticum urartu*) and its comparison with durum wheats. Australian Journal of Agricultural Research 59: 906-910.
10807.	Gao X, Appelbee MJ, Mekuria GT, Chalmers KJ & Mather DE Two different x-type glutenin subunits encoded by a novel allele at the *Glu-B1* locus of wheat (submitted).
10808.	Liu L, Wang A, Appels R, Ma J, Xia X, Lan P, He Z, Bekes F, Yan Y & Ma W 2009 A MALDI-TOF based analysis of high molecular weight glutenin subunits for wheat breeding. Journal of Cereal Science 50: 295-301.

10809.	Carmona S, Alvarez JB & Caballero L 2010 Genetic diversity for morphological traits and seed storage proteins in Spanish rivet wheat. Biologia Plantarum 54: 69-75.
10810.	Caballero L, Peña RJ, Martín LM & Alvarez JB 2010 Characterization of Mexican Creole wheat landraces in relation to morphological characteristics and HMW glutenin subunit composition. Genetic Resources and Crop Evolution 57: 657-665.
10811.	Martín MA, Martín LM & Alvarez JB 2008 Polymorphisms at the *Gli-A^{u}1* and *Gli-A^{u}2* loci in wild diploid wheat (*Triticum urartu*). Euphytica 163: 303-307.
10812.	Ma DY, Yan J, He ZH, Wu L & Xia XC 2011 Characterization of a cell wall invertase gene *TaCwi-A1* on common wheat chromosome 2A and development of functional markers. Molecular Breeding, DOI 10.1007/s11032-010-9524-z.
10813.	Appelbee MJ 2011 Personal communication.